

FIGURE 1

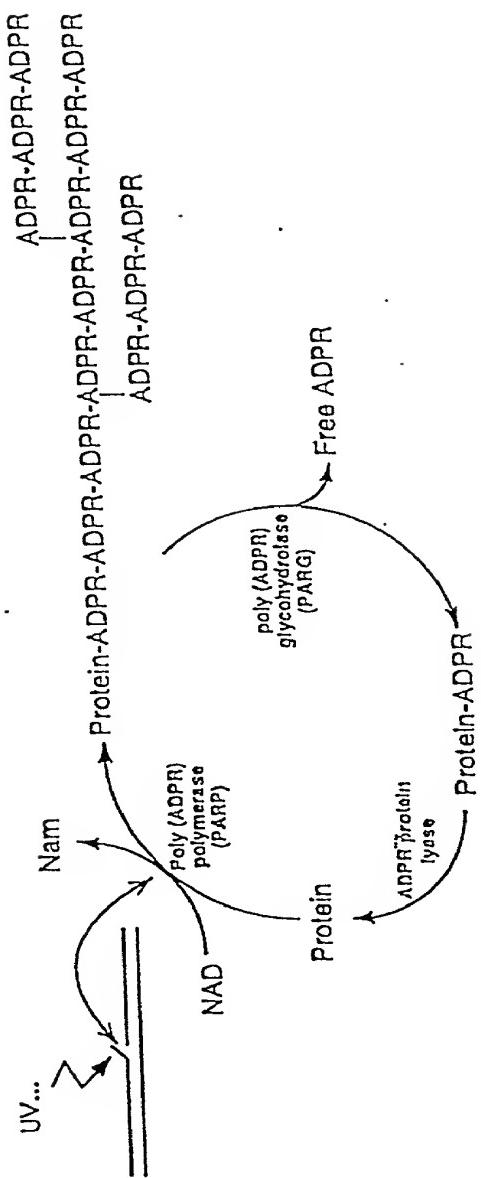


FIGURE 2

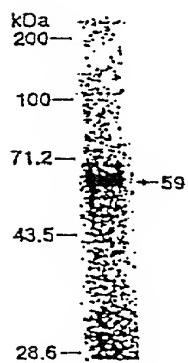


FIGURE 3

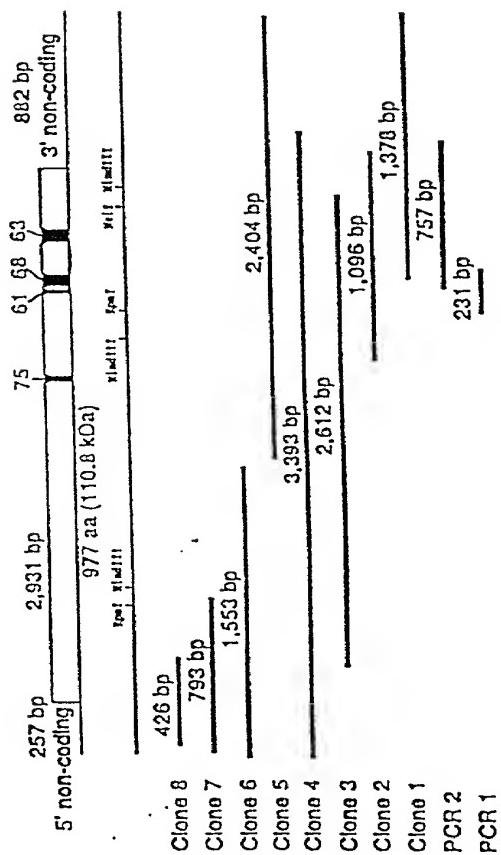


FIGURE 4

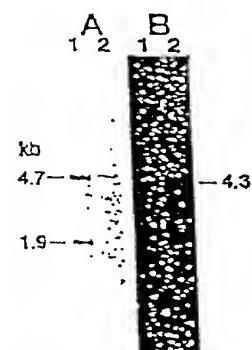


FIGURE 5

bPARG	(422)	ED. . . KRKEQCEMKHQRT. . RKİPKYIİPPH SEQ ID NO: 19
hPARG	(421)	ED. . . RRKEQWETKHQRT. . RKİPKYVPPH SEQ ID NO: 20
mPARG	(413)	ED. . . RRKEQCEVRHQRT. . RKİPKYIİPPN SEQ ID NO: 21
CePARG	(29)	HQVPTMKRRLTEHGNNTTESLLKLKDPEEPKS SEQ ID NO: 22
hPARP	(205)	EG. . . KRKGD. EVDG. VDEVAKKKSKKEKDK SEQ ID NO: 23
mPARP	(205)	EG. . . KRKGD. EVDG. TDEVAKKKSRKETDK SEQ ID NO: 24
bPARP	(208)	EG. . . KRKGD. EVDG. IDEVTKKKSKKEKDK SEQ ID NO: 25
aPARP	(205)	EG. . . KRKG. EVDG. . MVVAKKKSRKEKEK SEQ ID NO: 26
xIPARP	(204)	EG. . . KRKAD. EVDG. HSAATKKKKKEKEK SEQ ID NO: 27
DmPARP	(202)	EELPDTKRAKM. ELSDTNEEGEKKQR. SEQ ID NO: 28
SpPARP	(205)	EGVSSSAKKAKI. EKIDEEADAASIKELEKIKK SEQ ID NO: 29

FIGURE 6

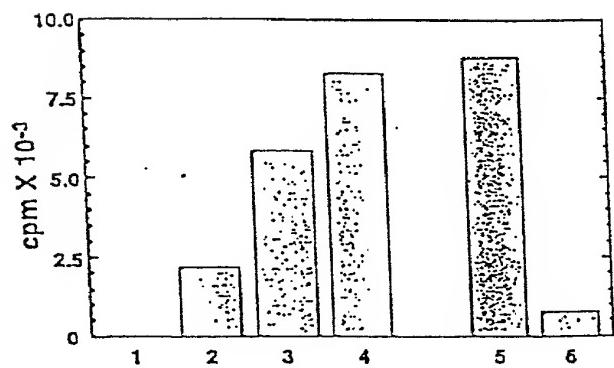


FIGURE 7

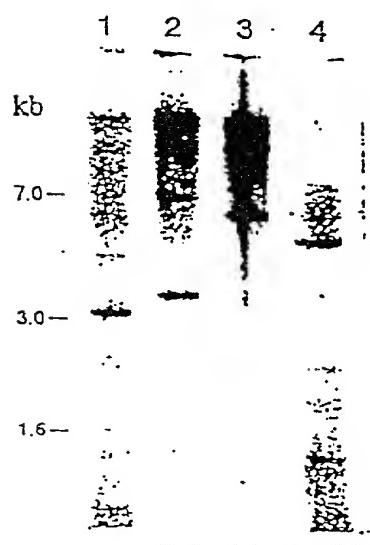


FIGURE 8

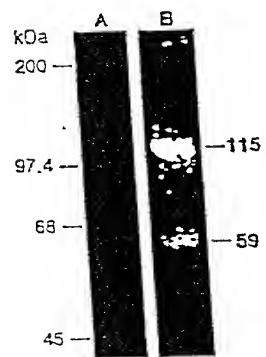


FIGURE 9

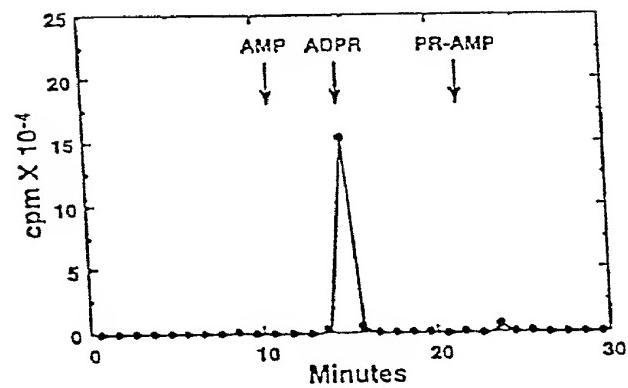


FIGURE 10

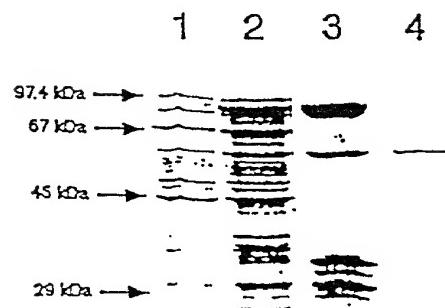


FIGURE 11

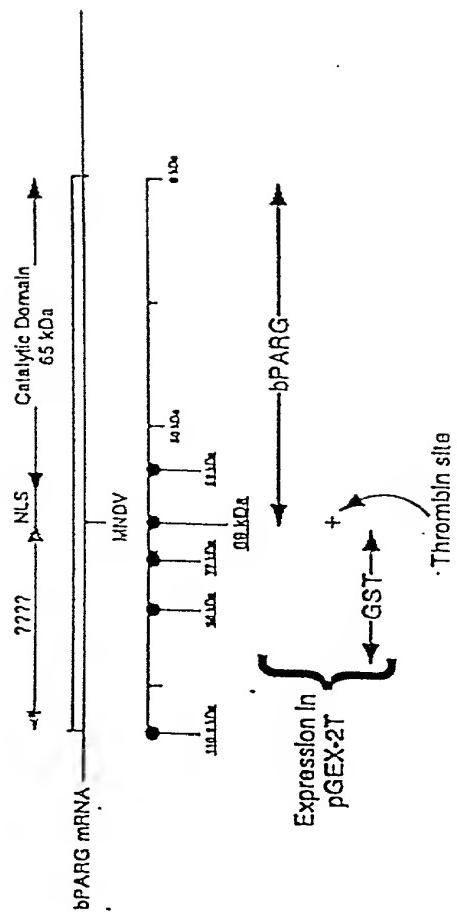


FIGURE 12

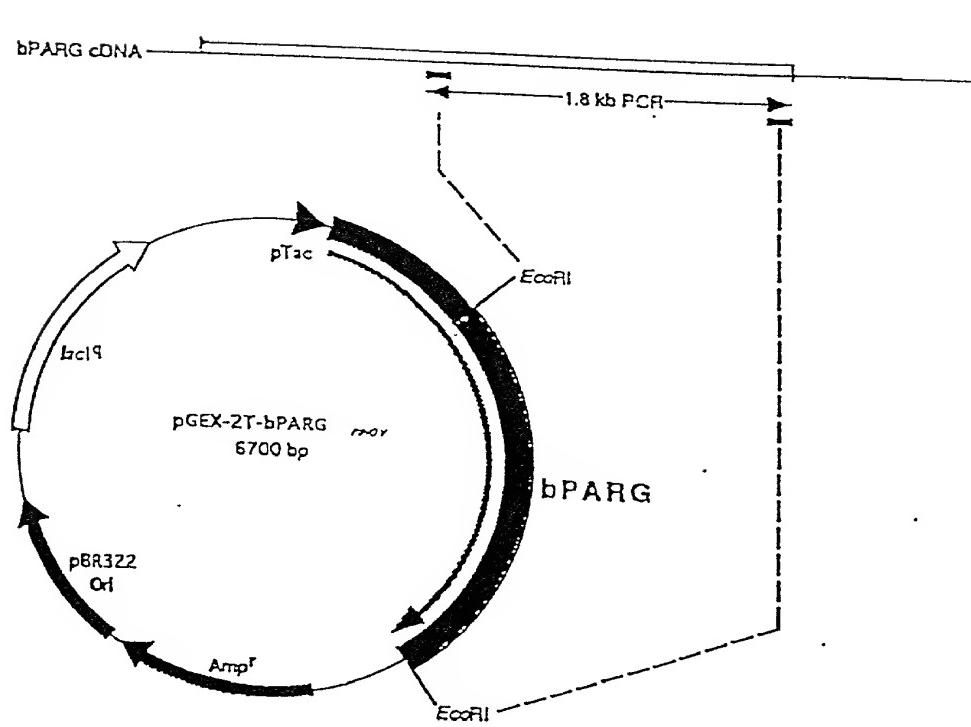


FIGURE 13

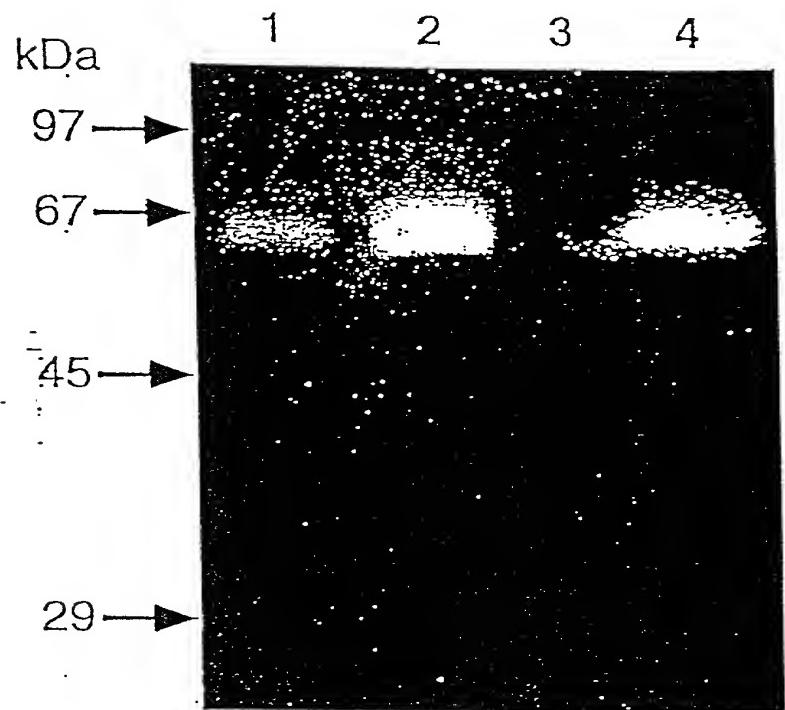
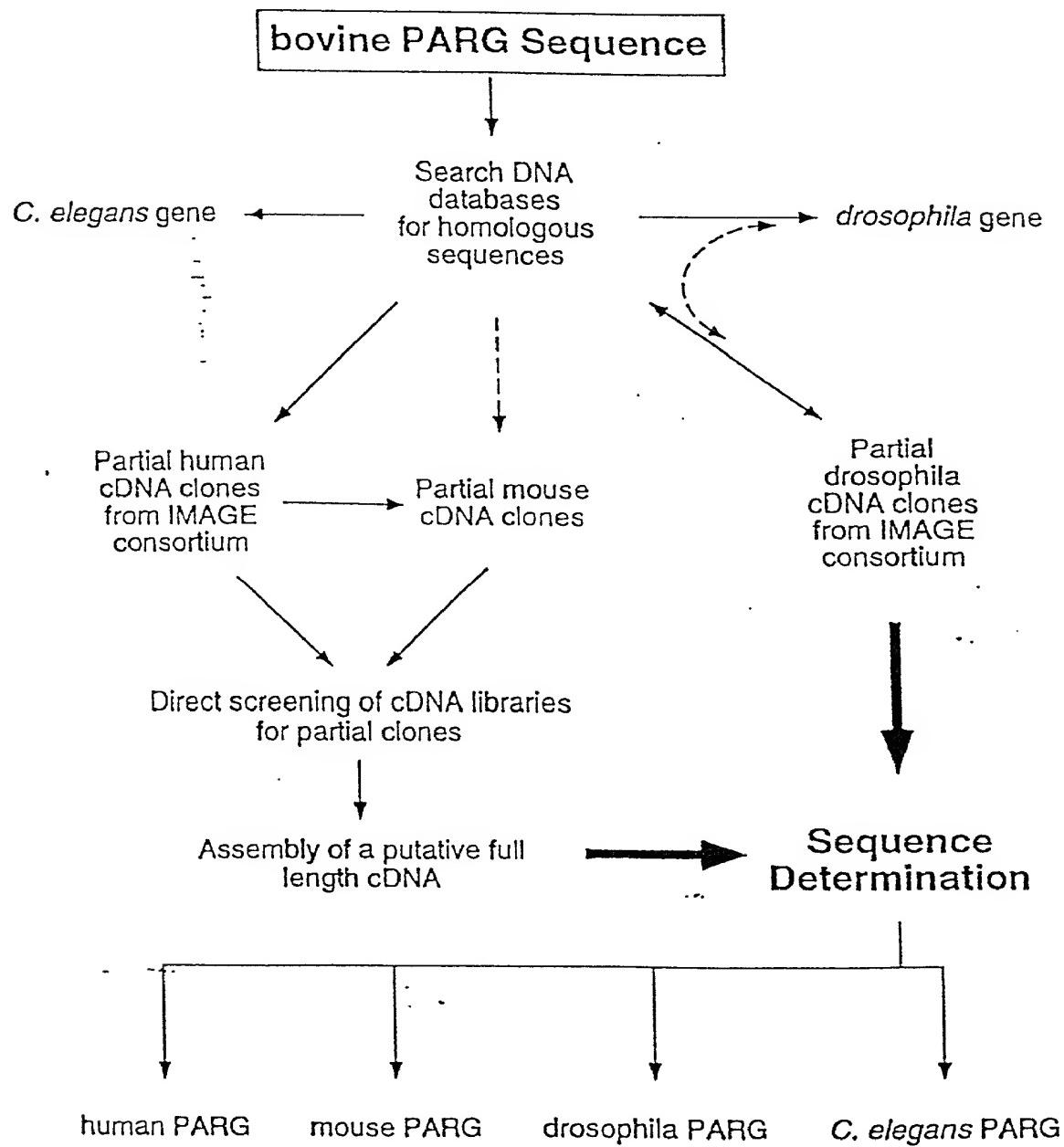


FIGURE 14

Strategy to Obtain Homologous PARG Sequences



Domain Organization of PARGs

FIGURE 15

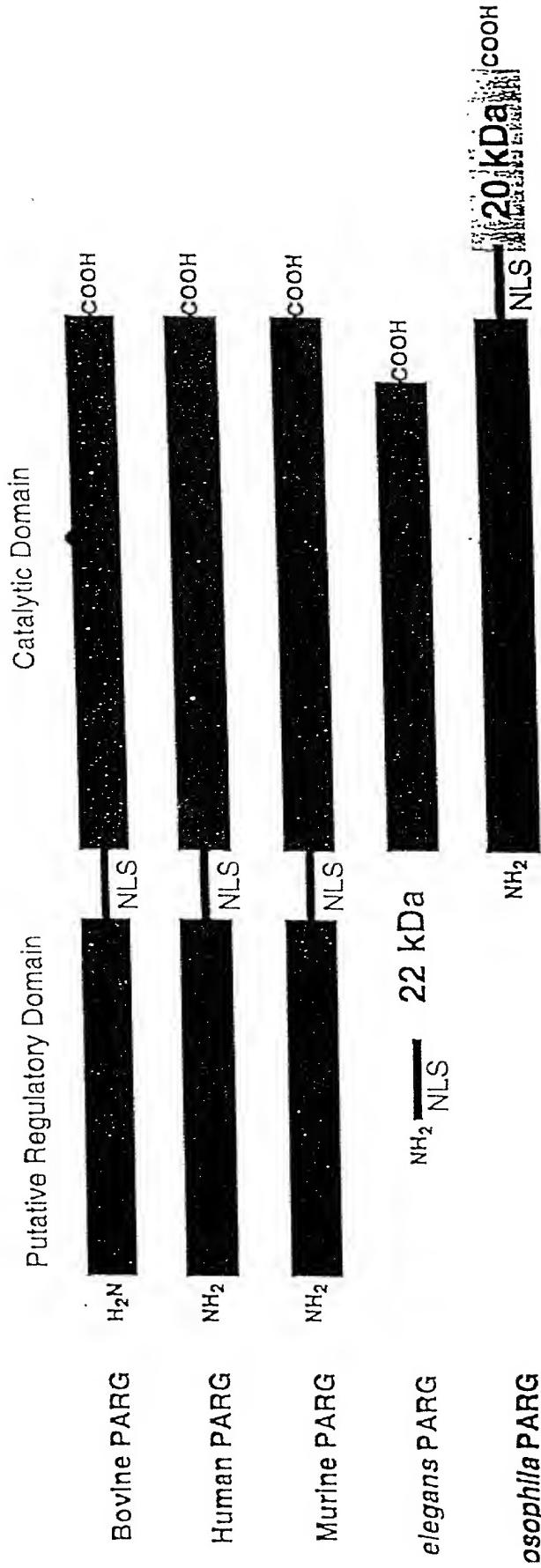


FIGURE 16

Multiple Alignment of Amino Acid Sequences of PARG from Different Species

```

parg      1  MSAGFGCEPCTRRPRWDAAARTSPPAASDARSFFPGRQRRLVLDSDRADPVQFRVFPSSSGCALGRAGQERGSATSLVFQKORTITSWMDTRGIKTVESSESLESK
parg      1  MNAAGPGCEPCTKATRWGATTs. PAASDARSPPSRQRRLVLDPRDAHVQFRVFPSSFACVFGQAGQERGSATSLVFQKORTITSWMDTRGIRTAESLDSK
parg      1  MSAGFGWEPCDKA. RNGAAGTSAPTAASDRSFPPGRQRRLVLDPKDAPVQFRVFPSSFACVSGRAGPERGNATSFVFKQRTITTWMDTRGFRTAESE...SR
parg      1  -----
eparg     1  ----

parg      101 EHHNNTREESMMSSVQKDHFYQHNMKELEHVSQQLGFDKSPVEKGTQYLKQEQTAAACWKQNEGPESERLLESEPPAVTLVPEQFSNANVDQSSPRDDHESDT
parg     100 EHHNNTRIESMMSSVQKDHFYQHNVKEVLNVSQLSLDRSLTEKSTQYLNQEQTAAACRKQNEGKETEQLLESEFQTVTLVPEQFSNANIDRSPONDDESDT
parg      97 EHHNTRIDSMMSSVQRDHFYPEKVEKLENVQLNLDSPTEXSSQYLNQQQTASVCKWQNEGREAEQLLASEFFAGTFLPRQLSNANIGQSPETDDESDT
parg      1  -----
eparg     1  ----

parg      1  MSKKFIELGDPVHQDEKD18DY
parg      101 EHHNNTREESMMSSVQKDHFYQHNMKELEHVSQQLGFDKSPVEKGTQYLKQEQTAAACWKQNEGPESERLLESEPPAVTLVPEQFSNANVDQSSPRDDHESDT
parg     100 EHHNNTRIESMMSSVQKDHFYQHNVKEVLNVSQLSLDRSLTEKSTQYLNQEQTAAACRKQNEGKETEQLLESEFQTVTLVPEQFSNANIDRSPONDDESDT
parg      97 EHHNTRIDSMMSSVQRDHFYPEKVEKLENVQLNLDSPTEXSSQYLNQQQTASVCKWQNEGREAEQLLASEFFAGTFLPRQLSNANIGQSPETDDESDT
parg      1  -----
eparg     1  ----

parg      201 NSEESRDNQQPLTHVXL...ANAKQTMEDEQGREALRSHQRCGXACHFAEACAGCQQEEEDVUVSESPLSLSDTGSEDVTGLKXHANRLNRQESSLGNSPPFER
parg     200 DSEENRDNQQPLTUVXL...ANAKQTTEDEHAREAKSEQPKCSKSCFEDCASCQDIDVVFRSPSLDVGSEDVTGSKNDNLKIRQESCLGNSPPFEK
parg      197 DHEEDRDNQQPLTPIKL...ANTKPTVGDGQ...ARSNCKCSGSRSQVKDCTGCQQUEEVDVLPESPSLSDVGAEDITGPKNDNLKTGQESSLGNSPPFEK
parg      1  -----
eparg     23 VGVGFHQVPTMRRKLTEEGNTTESREDPEEPKSRSDFVFSQSSDESQEDSAENPEIAKEVSENCENLTELKISNIESLDNVTERSEHTLDN...EK

parg      298 ESEPESPMDVDNSKNSCQDSEADDEETSPGFDE..QEDSSSAQTAHKPSRFQPREADTELRKRSSAKGGEIRLEFQPEGGESRAQHN..DVMARRGSTSSLN
parg     297 ESEPESPMDVDNSKNSCQDSEADEETSPGFDE..QEDGSSSQTAAHRPSRFQARDADIEFRRYSTRGGEVRLFQPEGGESRTQHN..DLNAKLPONISSLN
parg     291 ESEPESPMDVDSRNSKNSCQDSEADEETSPVFDE..QDDRSS..QTAHRLSSCQAREADGDLRKRYLTKGSEVRLEFQFE..GENNAGTS..DLNAKPSGNSSLN
parg      1  -----
eparg     119 STEPMEE..DVNNRSHIDVAINSDEDDELVLEENHKEHRDGEQVQQLS..QDLFADDQELIYEPGIMKDTTTQLDITDSEVETAQKMEMIEETADSTFVG

parg      396 VECRNSKQEGGRKDSRITDHFMRVPKAEDKRKEQCEMKERQTERTRIPKYYIPFHLSPDKEENLGTPIEM..RRMPRCGIRLFPLRPSANETVTIRV DLLRIG
parg     395 VECRNSKQEGGKDKDSKITDHLMRLPKAEDRRKEQNETKEERTERKIPKXXVPPELSPDKEENLGTPIEM..RRMPRCGIRLPPLRPSANETVTIRV DLLRAG
parg     387 VECRNSKQEGKRDMSKTEDHFMRIKSKSEDRRKEQCEVRHQERTERKIPKXXVPPEKKNLGTPIEM..RRMPRCGIRLFPLRPSASETVTVRV DLLRAG
parg      32 ...TNRLGR...ALCLNCARMSKSFDDGGISEK...TEEE..PEHLANSL..DWSRGVSMSAIERNRQPPELENLFPVAGNLERVMYQLPIRET.
Ceparg    216 EDSKATKTVTSSSS...LSTVSTCCEAPAKGRARMYQRELEREVIATEGMLT...LQPDLNRPDPDRNHYR..CTIPNFPASQG...RLRED..NRIG

parg      494 EVPR..PPFTFPLDWDNKEVVKFCSEQNLYPVEDENGE..RAAGSRWELIQTALLNRLTRFQNLKDAILKYNVAYSRRWDFTALIDFWDRVLEEAQELY
parg     493 EVPK..PPFTEYKDLWDNKEVVKFCSEQNLYPVEDENGE..RTAGSRWELIQTALLNKFTRFQNLKDAILRNVAYSRRWDFTALIDFWDRVLEEAQELY
parg     485 EVPK..PPFTHYRDLWDNKEVVKFCSEQNLYPVEDENGE..RTAGSRWELIQTALLNTRFQNLKDAILRNVAYSRRWDFTALIDFWDRVLEEAQELY
Dparg     115 .PPR..PYRSPGK..WDSSEEVRLPCAPESRYPRENFDSG..TTIDFRWNEMIERRALQPKTCBLLQRAIYTSINTTIRDQWHFRALHQLLDEEDESETRVFF
Ceparg    303 ..PKIVLPQRWR..FDSRGRR...RDSYFYFRRKLGDYLCKYTGYMFVGCLL.....NMWE..FDFDITYR...LPAL..EMYKEMSELVGREEV

parg      592 QSIPLDMVKIALCLPNICTQFIPLLKQKMNESITMSQEQIASLLANAFFCTFFF RNA..RMRSEYSSYPDINFNRRLFEGRSSRKPPEKLTKLFCYFRRV..T
parg     591 QSIPLDMVKIALCLPNICTQFIPLLKQKMNESITMSQEQIASLLANAFFCTFFF RNA..KMKSEYSSYPDINFNRRLFEGRSSRKPPEKLTKLFCYFRRV..T
parg     583 QSIPLDMVKIALCLPNICTQFIPLLKQKMNESITMSQEQIASLLANAFFCTFFF RNA..KMKSEYSSYPDINFNRRLFEGRSSRKPPEKLTKLFCYFRRV..T
Dparg    210 EDLPLPRIIRALRALKPLDIQSPVPLKKHKNASLSSQQQISCLLANAFLCTFPFRNLTKRKSEISTFPDINFNRLYGSTGPAVLERLKCIMHYFRRVCPT
Ceparg    384 LEKFARVARIAKTAEDILPERIYRLVGDVE..SATLSEKCAALVARMFA.....RPDSPFS....FCRILSSDRSICVERLKFLPTYF.....
parg      689 EKK....PTGLVTFTRQS..L..ED..F..PEWERCEKLL..TRLHVTYEGTIEGNGQGMLQVDFANRFLVGGGVTSAGLVQEERFLINPELIVSRLPTEVLDH
parg     688 EKK....PTGLVTFTRQS..L..ED..F..PEWERCEKPL..TRLEVTVEGTIEGNGQGMLQVDFANRFLVGGGVTSAGLVQEERFLINPELIVSRLPTEVLDH
parg     680 EKK....PTGLVTFTRQS..L..ED..F..PEWERCEEPL..TRLEVTVEGTIEGNGQGMLQVDFANRFLVGGGVTAGLVQEERFLINPELIVSRLPTEVLDH
Dparg    310 ERDASNVPVGVTFRSGLPEE..L..IDWSQSAAPLGDPVLEVDAGETIEDEGIGLQVDFANRFLVGGGVLGHGCVQEIRFVICPELUVGKLFTECLRP
Ceparg    463 DKMMSMDPPDGAVSF..RLTRMDRDTFNEEW..KDRRLRLSLSLFEVEFFDEMILIEDLT..CTQVDPFANEELGGGVLNHEGSVQEERFLMCPEKXMGHLLCEKMKQ

parg      779 HECLIIITGTEQSYTGYAETIRWA....RSEEDRSE..RDDWQRRRTTEIVAI DALHFR..RYLD....QFVFERIRRELNKAYCGFLRPGVSSENLSAVA
parg     778 HECLIIITGTEQSYTGYAETIRWA....RSEEDGSE..RDDCERRCTEIVAI DALHFR..RYLD....QFVFERIRRELNKAYCGFLRPGVSSENLSAVA
parg     770 HECLIIITGTEQSYTGYAETIRWA....RSEEDGSE..KDDWQRRCTEIVAI DALHFR..RYLD....QFVFERIRRELNKAYCGFLRPGVSSENLSAVA
Dparg    408 FEALVMLGAERIISNYTGYAGSFENS....GPFEDSTP..RDSGGRRQRTAIVAI DALHFR..QSH...QIREDLMERELNKAYIGFVENVVTPP..PGVA
Ceparg    560 LEAISIVGAYFSSSYTGYGETLKWAELQPNESRQNTNEFRDPRGRLRVTETIAIDALFLRGSKLDQTLQLNKANIIREMREASIGFMSQGKFTHIP..IV

parg      868 TGNWCGCAFGGDARLKLAKIQLIQLAAAVERDVVIFTFGDSELMDRDIYSMETHPLTERKLTVGE..VYKLLRLRYINEECRNCTSTPGF.....DIKLYPFIYEA
parg     867 TGNWCGCAFGGDARLKLAKIQLIQLAAAVERDVVIFTFGDSELMDRDIYSMETHPLTERKLTVGD..VYRLLRLRYINEECRNCTSTPGF.....DIKLYPFIYHA
parg     859 TGNWCGCAFGGDARLKLAKIQLIQLAAAVERDVVIFTFGDSELMDRDIYSMETHPLTERKLTVGD..VYKLLRLRYINEECRNCTSTPGF.....DIKLYPFIYHA
Dparg    495 TGNWCGCAFGGDARLKLAKIQLIQLAAAVERDVVIFTFGDSELMDRDIYSMETHPLTERKLTVGD..VYKLLRLRYINEECRNCTSTPGF.....DIKLYPFIYHA
Ceparg    659 TGNWCGCAFNGDKFLKFITQVIAAGVADRFPLHFCSPGEPELAACKRIIERMKQKDVTLGKSCFSYF-----

parg      961 VESCTQTTNQPGQRTGA-----
parg     960 VESCATADESGQRTGT-----
parg     952 VESSAETTDMFQGKAGT-----
Dparg    590 KEELKKVVRDVPGEGASAEAGSSRVAAGLGEKGKSETSAKSSPELNKQFARPQITITQQSTDLLPAQLSQDNNSSEDQALLMLSDEEANAMHEASLEAKS
Ceparg    727 ----

parg      978 -----
parg     977 -----
parg     969 -----
Dparg    690 SVEISNSSTSRTSSTATRSMGSGRQLSLLMLDTHYEKG SASKRPRKSPNC SKAEGSAKS RREIDVTDKDERDDIVD
Ceparg    727 -----

```

FIGURE 17

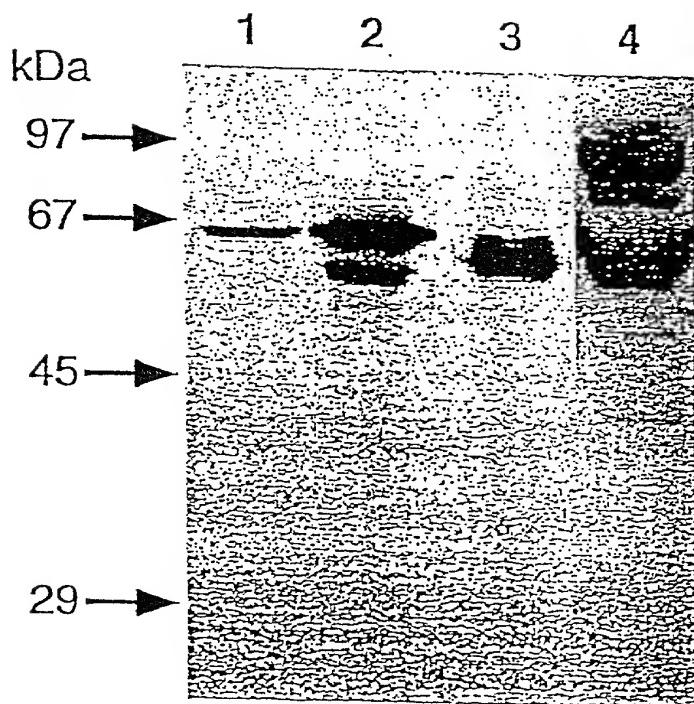
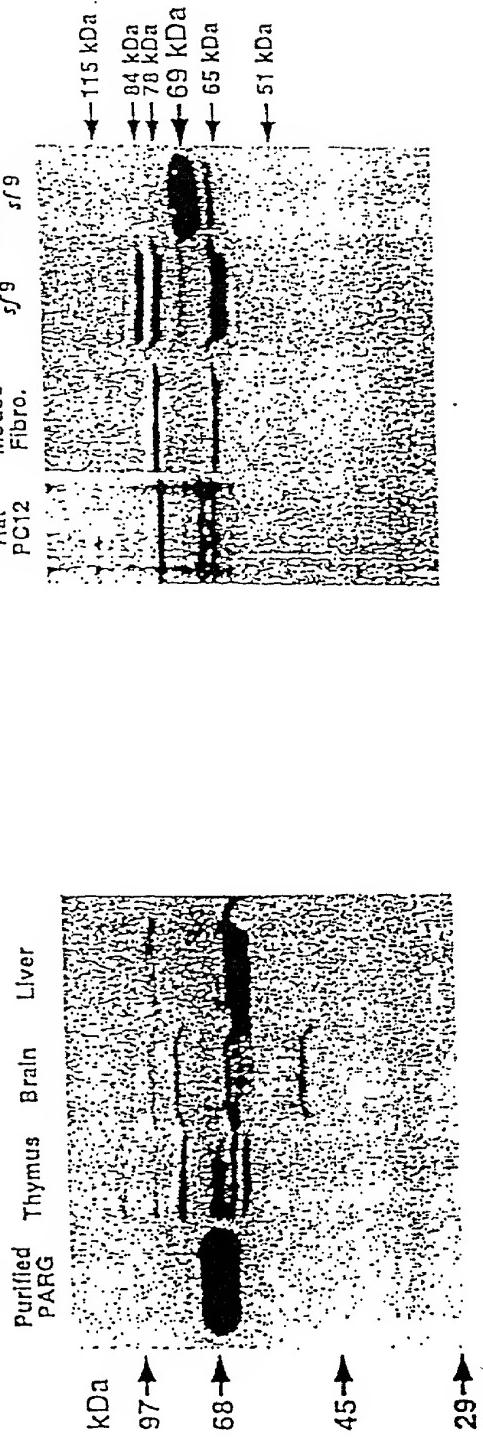


FIGURE 18

Bovine Tissue Cell Extracts



A

B

FIGURE 19

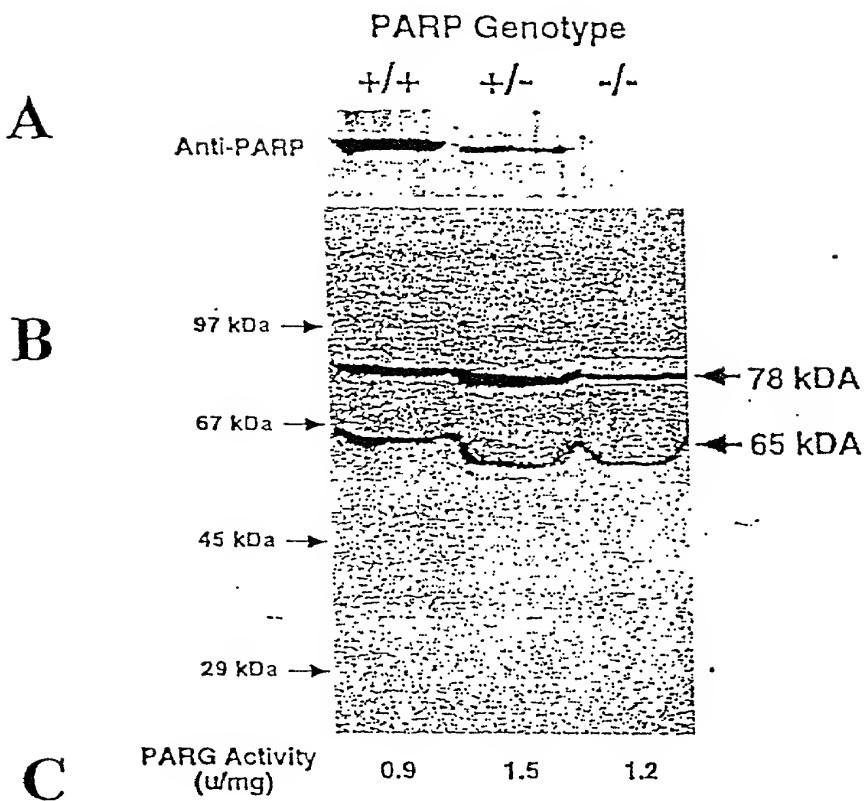


FIGURE 20

Genomic cloning of the PARG gene

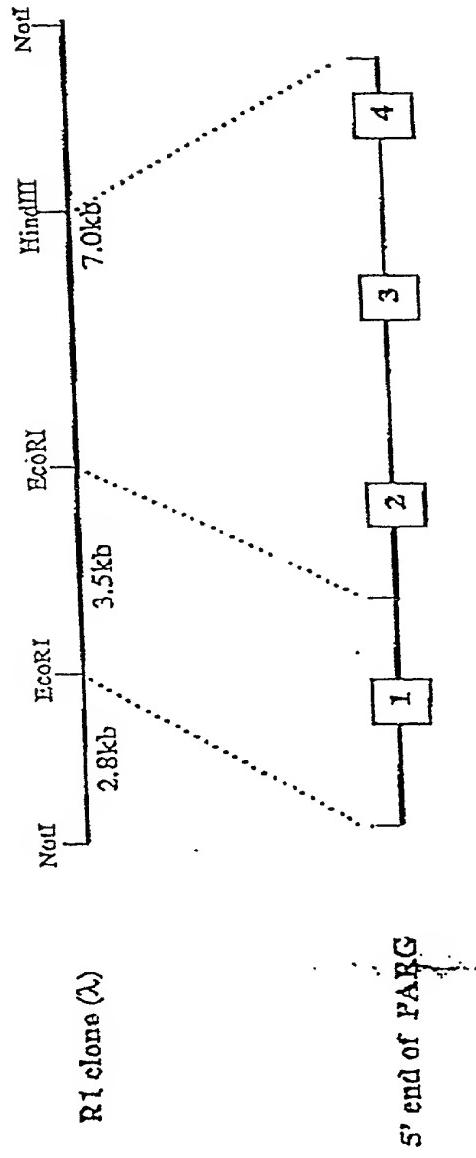


FIGURE 21

